SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: HÖTTEN, Gertrud
                NEIDHARDT, Helge
                BECHTOLD, Rolf
                POHL, Jens

    (ii) TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
          GROWTH/DIFFERENTIATION FACTORS

    (iii) NUMBER OF SEQUENCES: 6

    (iv) CORRESPONDENCE ADDRESS:
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           Suite 330
        (C) CITY: Washington
        (D) STATE: DC
        (E) COUNTRY: USA
        (F) ZIP: 20005

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: UNKNOWN
        (B) FILING DATE: 12-JUL-1996
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: KLESNER, Sharon N
        (B) REGISTRATION NUMBER: 36,335
        (C) REFERENCE/DOCKET NUMBER: P564-5010

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 202/638-5000
        (B) TELEFAX: 202/638-4810

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2272 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CAAGGAGCCA TGCCAGCTGG ACACACACTT CTTCCAGGGC CTCTGGCAGC CAGGACAGAG      60

TTGAGACCAC AGCTGTTGAG ACCCTGAGCC CTGAGTCTGT ATTGCTCAAG AAGGGCCTTC     120

CCCAGCAATG ACCTCCTCAT TGCTTCTGGC CTTTCTCCTC CTGGCTCCAA CCACAGTGGC     180

CACTCCCAGA GCTGGCGGTC AGTGTCCAGC ATGTGGGGGG CCCACCTTGG AACTGGAGAG     240

CCAGCGGGAG CTGCTTCTTG ATCTGGCCAA GAGAAGCATC TTGGACAAGC TGCACCTCAC     300

CCAGCGCCCA ACACTGAACC GCCCTGTGTC CAGAGCTGCT TTGAGGACTG CACTGCAGCA     360

CCTCCACGGG GTCCCACAGG GGGCACTTCT AGAGGACAAC AGGGAACAGG AATGTGAAAT     420

CATCAGCTTT GCTGAGACAG CCTCTCCAC CATCAACCAG ACTCGTCTTG ATTTTCACTT     480

GTCCTCTGAT AGAACTGCTG GTGACAGGGA GGTCCAGCAG GCCAGTCTCA TGTTCTTTGT     540

GCAGCTCCCT TCCAATACCA CTTGGACCTT GAAAGTGAGA GTCCTTGTGC TGGGTCCACA     600

TAATACCAAC CTCACCTTGG CTACTCAGTA CCTGCTGGAG GTGGATGCCA GTGGCTGGCA     660

TCAACTCCCC CTAGGGCCTG AAGCTCAAGC TCCCTGCAGC CAGGGGCACC TGACCCTGGA     720

GCTGGTACTT GAAGGCCAGG TAGCCCAGAG CTCAGTCATC CTGGGTGGAG CTGCCCATAG     780

GCCTTTTGTG GCAGCCCGGG TGAGAGTTGG GGGCAAACAC CAGATTCACC GACGAGGCAT     840

CGACTGCCAA GGAGGGTCCA CGATGTGCTG TCGACAAGAG TTTTTTGTGG ACTTCCGTGA     900

GATTGGCTGG CACGACTGGA TCATCCAGCC TGAGGGCTAC GCCATGAACT TCTGCATAGG     960

GCAGTGCCCA CTACACATAG CAGGCATGCC TGGTATTGCT GCCTCCTTTC ACACTGCAGT    1020

GCTCAATCTT CTCAAGGCCA ACACAGCTGC AGGCACCACT GGAGGGGGCT CATGCTGTGT    1080

ACCCACGGCC CGGCGCCCCC TGTCTCTGCT CTATTATGAC AGGGACAGCA ACATTGTCAA    1140

GACTGACATA CCTGACATGG TAGTAGAGGC CTGTGGGTGC AGTTAGTCTA TGTGTGGTAT    1200

GGGCAGCCCA AGGTTGCATG GGAAAACACG CCCCTACAGA AGTGCACTTC CTTGAGAGGA    1260

GGGAATGACC TCATTCTCTG TCCAGAATGT GGACTCCCTC TTCCTGAGCA TCTTATGGAA    1320

ATTACCCCAC CTTTGACTTG AAGAAACCTT CATCTAAAGC AAGTCACTGT GCCATCTTCC    1380
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TGACCACTAC CCTCTTTCCT AGGGCATAGT CCATCCCGCT AGTCCATCCC GCTAGCCCCA     1440

CTCCAGGGAC TCAGACCCAT CTCCAACCAT GAGCAATGCC ATCTGGTTCC CAGGCAAAGA     1500

CACCCTTAGC TCACCTTTAA TAGACCCCAT AACCCACTAT GCCTTCCTGT CCTTTCTACT     1560

CAATGGTCCC CACTCCAAGA TGAGTTGACA CAACCCCTTC CCCCAATTTT TGTGGATCTC     1620

CAGAGAGGCC CTTCTTTGGA TTCACCAAAG TTTAGATCAC TGCTGCCCAA AATAGAGGCT     1680

TACCTACCCC CCTCTTTGTT GTGAGCCCCT GTCCTTCTTA GTTGTCCAGG TGAACTACTA     1740

AAGCTCTCTT TGCATACCTT CATCCATTTT TTGTCCTTCT CTGCCTTTCT CTATGCCCTT     1800

AAGGGGTGAC TTGCCTGAGC TCTATCACCT GAGCTCCCCT GCCCTCTGGC TTCCTGCTGA     1860

GGTCAGGGCA TTTCTTATCC CTGTTCCCTC TCTGTCTAGG TGTCATGGTT CTGTGTAACT     1920

GTGGCTATTC TGTGTCCCTA CACTACCTGG CTACCCCCTT CCATGGCCCC AGCTCTGCCT     1980

ACATTCTGAT TTTTTTTTTT TTTTTTTTTT TGAAAAGTTA AAAATTCCTT AATTTTTTAT     2040

TCCTGGTACC ACTACCACAA TTTACAGGGC AATATACCTG ATGTAATGAA AAGAAAAAGA     2100

AAAAGACAAA GCTACAACAG ATAAAAGACC TCAGGAATGT ACATCTAATT GACACTACAT     2160

TGCATTAATC AATAGCTGCA CTTTTTGCAA ACTGTGGCTA TGACAGTCCT GAACAAGAAG     2220

GGTTTCCTGT TTAAGCTGCA GTAACTTTTC TGACTATGGA TCATCGTTCC TT            2272
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 352 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (x) PUBLICATION INFORMATION:
        (H) DOCUMENT NUMBER: US 08/289,222
        (I) FILING DATE: 12-AUG-1994

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Thr Ser Ser Leu Leu Leu Ala Phe Leu Leu Leu Ala Pro Thr Thr
1               5               10              15

Val Ala Thr Pro Arg Ala Gly Gly Gln Cys Pro Ala Cys Gly Gly Pro
                20              25              30
```

```
Thr Leu Glu Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
         35                  40                  45

Arg Ser Ile Leu Asp Lys Leu His Leu Thr Gln Arg Pro Thr Leu Asn
         50              55                  60

Arg Pro Val Ser Arg Ala Ala Leu Arg Thr Ala Leu Gln His Leu His
65              70                  75                      80

Gly Val Pro Gln Gly Ala Leu Leu Glu Asp Asn Arg Glu Gln Glu Cys
             85                  90                  95

Glu Ile Ile Ser Phe Ala Glu Thr Gly Leu Ser Thr Ile Asn Gln Thr
             100                 105                 110

Arg Leu Asp Phe His Phe Ser Ser Asp Arg Thr Ala Gly Asp Arg Glu
         115             120                 125

Val Gln Gln Ala Ser Leu Met Phe Phe Val Gln Leu Pro Ser Asn Thr
     130             135                 140

Thr Trp Thr Leu Lys Val Arg Val Leu Val Leu Gly Pro His Asn Thr
145             150                     155                 160

Asn Leu Thr Leu Ala Thr Gln Tyr Leu Leu Glu Val Asp Ala Ser Gly
             165                 170                 175

Trp His Gln Leu Pro Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
             180                 185                 190

Gly His Leu Thr Leu Glu Leu Val Leu Glu Gly Gln Val Ala Gln Ser
         195                 200                 205

Ser Val Ile Leu Gly Gly Ala Ala His Arg Pro Phe Val Ala Ala Arg
     210             215                 220

Val Arg Val Gly Gly Lys His Gln Ile His Arg Arg Gly Ile Asp Cys
225             230                 235                     240

Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
             245                 250                 255

Arg Glu Ile Gly Trp His Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
             260                 265                 270

Met Asn Phe Cys Ile Gly Gln Cys Pro Leu His Ile Ala Gly Met Pro
         275             280                 285

Gly Ile Ala Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
     290             295                 300

Asn Thr Ala Ala Gly Thr Thr Gly Gly Gly Ser Cys Cys Val Pro Thr
```

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```
     305                    310                      315                   320
      |   |      |      |                                           |    |
     Ala Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
                     325                 330                   335
      |           |     |                                          |
     Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
                     340                 345                   350
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1558 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

    (x) PUBLICATION INFORMATION:
        (H) DOCUMENT NUMBER: US 08/289,222
        (I) FILING DATE: 12-AUG-1994

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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AAGGAGTCAT GCCAGTCGGA GGTCAGTCAC ATTCCTCCCA GGGTCCCTGG TGCCCAGGAC   60

AGAGTTGAAG CACTCCCGTT GAGACCCTGA ATATAGGCTT TGGGTCCTTT AAGGAGGCTA  120

TCCTCCAGCA ATGGCCTCCT CCTTGCTCCT GGCTCTTCTG TTCCTGACTC CAACCACAGT  180

AGTGAACCCC AAAACTGAGG GTCCATGCCC AGCATGTTGG GGTGCCATCT TTGACCTGGA  240

GAGCCAGCGG GAGCTGCTTC TCGATTTGGC CAAGAAAGT ATCCTGGACA AGCTGCACCT  300

CAGCCAGCGC CCCATACTCA GTCGGCCAGT GTCCAGAGGG GCTCTCAAGA CCGCGCTGCA  360

GCGCCTCCGC GGGCCTCGAC GGGAAACCCT GTTGGAGCAT GACCAGAGAC AAGAAGAATA  420

TGAGATCATC AGCTTTGCTG ACACAGACCT CTCCAGCATC AACCAGACCC GGCTCGAGTT  480

CCACTTCTCT GGTAGAATGG CCAGTGGCAT GGAGGTCCGG CAGACCCGCT TCATGTTCTT  540

CGTGCAGTTC CCCCACAATG CCACCCAGAC CATGAATATA AGAGTTCTTG TGCTAAGACC  600

ATATGACACC AACCTCACCT TGACAAGTCA GTACGTGGTG CAGGTGAATG CCAGTGGCTG  660

GTACCAGCTT CTCCTGGGAC CTGAAGCTCA AGCTGCTTGC AGCCAGGGAC ACCTTACTCT  720

GGAGCTGGTA CCAGAAAGCC AGGTGGCCCA CAGTTCCTTG ATCCTGGCCT GGTTTTCCCA  780

CAGGCCTTTT GTGGCAGCCC AGGTAAGGGT TGAGGGCAAG CATCGGGTTC GCCGGCGAGG  840
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TATCGATTGC CAGGGGGGGT CCAGGATGTG CTGTCGACAA GAGTTTTTTG TAGACTTCCG   900

TGAGATTGGC TGGAATGACT GGATCATCCA GCCTGAAGGC TATGCCATGA ACTTCTGCAC   960

TGGGCAGTGC CCACTACATG TGGCAGGCAT GCCTGGCATC TCTGCCTCCT TTCACACTGC   1020

AGTGCTGAAT CTGCTCAAAG CCAACGCAGC TGCTGGCACC ACTGGCAGGG GCTCGTGCTG   1080

CGTGCCTACA TCTCGGCGCC CTCTGTCTTT GCTCTACTAT GACAGGGACA GCAACATTGT   1140

CAAGACGGAT ATACCTGACA TGGTGGTCGA GGCCTGCGGG TGTAGTTAGC TTATGGGTGA   1200

TACAGGCTGC CTGAGGTAGA ATGGCCTTCC TCAGGAAGGG AAACTCTGTT CCCACTTCTG   1260

TCCAGAATGG AAACACCTTT CTAAGCATGC AGACATCCCT CTGTGGACTT CAGGGGATCC   1320

ACCTCTAAAG AGAGTCACTA GTGACCAACA GCCTTTCTCT CTCCTGGGAC ATGGTTGACC   1380

CAGTACACCC ATCCTCAGCC TTAAGTTAGA GGCTAATCGA CTCCTACATA TATATGTCAT   1440

TTTGTCCTAG CAAACACCCC TTAGCTCCCC TTAGTCAACT ATGTAATCTA CTCTGCCTCC   1500

CTGACCCTGC CACCGGAAGG TTCCTATTCC ACGATGATAT GCCTTAGTGT CTCCCCTT   1558

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 352 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (x) PUBLICATION INFORMATION:
        (H) DOCUMENT NUMBER: US 08/289,222
        (I) FILING DATE: 12-AUG-1994

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ser Ser Leu Leu Leu Ala Leu Leu Phe Leu Thr Pro Thr Thr
1   5   10   15

Val Val Asn Pro Lys Thr Glu Gly Pro Cys Pro Ala Cys Trp Gly Ala
            20   25   30

Ile Phe Asp Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
            35   40   45

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Lys Ser Ile Leu Asp Lys Leu His Leu Ser Gln Arg Pro Ile Leu Ser
    50   55   60

Arg Pro Val Ser Arg Gly Ala Leu Lys Thr Ala Leu Gln Arg Leu Arg
65   70   75   80

Gly Pro Arg Arg Glu Thr Leu Leu Glu His Asp Gln Arg Gln Glu Glu
            85   90   95

Tyr Glu Ile Ile Ser Phe Ala Asp Thr Asp Leu Ser Ser Ile Asn Gln
            100   105   110

Thr Arg Leu Glu Phe His Phe Ser Gly Arg Met Ala Ser Gly Met Glu
        115   120   125

Val Arg Gln Thr Arg Phe Met Phe Phe Val Gln Phe Pro His Asn Ala
    130   135   140

Thr Gln Thr Met Asn Ile Arg Val Leu Val Leu Arg Pro Tyr Asp Thr
145   150   155   160

Asn Leu Thr Leu Thr Ser Gln Tyr Val Val Gln Val Asn Ala Ser Gly
            165   170   175

Trp Tyr Gln Leu Leu Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
        180   185   190

Gly His Leu Thr Leu Glu Leu Val Pro Glu Ser Gln Val Ala His Ser
    195   200   205

Ser Leu Ile Leu Gly Trp Phe Ser His Arg Pro Phe Val Ala Ala Gln
210   215   220

Val Arg Val Glu Gly Lys His Arg Val Arg Arg Arg Gly Ile Asp Cys
225   230   235   240

Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
            245   250   255

Arg Glu Ile Gly Trp Asn Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
            260   265   270

Met Asn Phe Cys Thr Gly Gln Cys Pro Leu His Val Ala Gly Met Pro
        275   280   285

Gly Ile Ser Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
    290   295   300

Asn Ala Ala Ala Gly Thr Thr Gly Arg Gly Ser Cys Cys Val Pro Thr
305   310   315   320

45

```
Ser Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
             325                     330             335

Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
             340                 345             350
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

    (x) PUBLICATION INFORMATION:
        (H) DOCUMENT NUMBER: US 08/289,222
        (I) FILING DATE: 12-AUG-1994

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
                                                              18
CAGGTAGGTC CATGGTCG
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 21
        (D) OTHER INFORMATION: /note= "XAA IS T OR C"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 27
        (D) OTHER INFORMATION: /note= "XAA IS A OR G"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 33
        (D) OTHER INFORMATION: /note= "XAA IS A, C, T OR G"

(x) PUBLICATION INFORMATION:
     (H) DOCUMENT NUMBER: US 08/289,222
     (I) FILING DATE: 12-AUG-1994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGATTTTT AACAGACC   18